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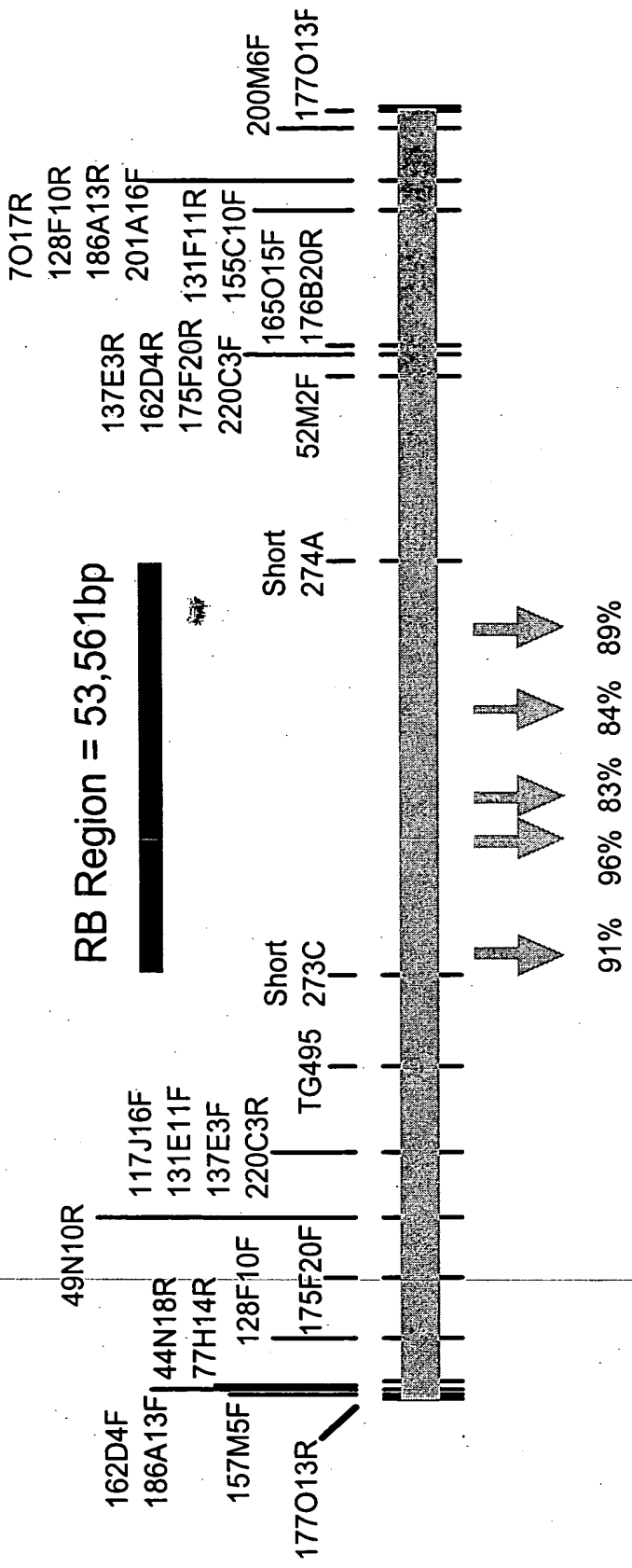
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Nucleotide Binding-Site/ Leucine Rich Repeat (NBS-LRR)

Fig. 2

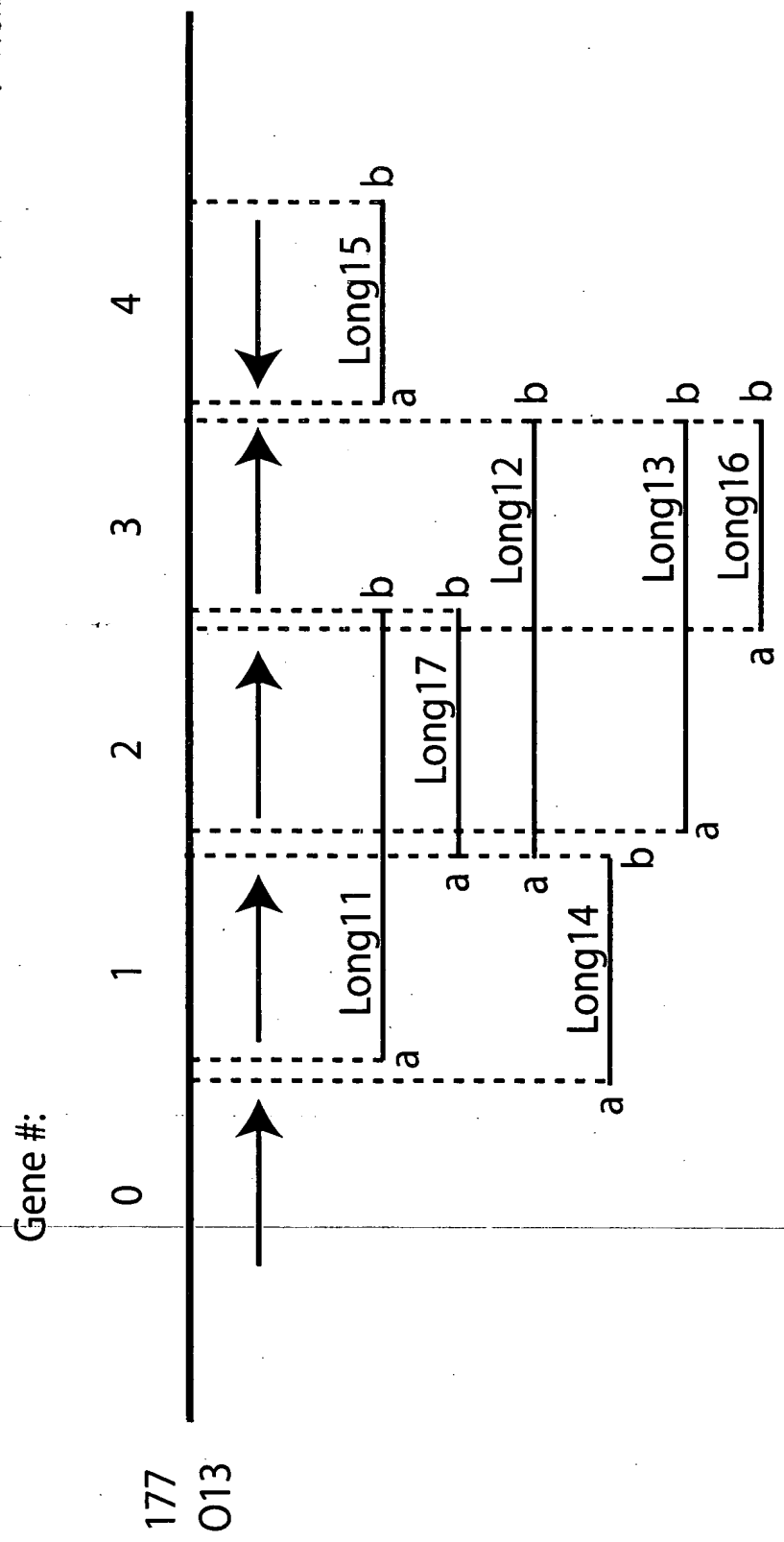


Fig.3

LRPCR Product Sizes

Long11	15,008bp
Long12	19,988bp
Long13	19,897bp
Long14	6,971bp
Long15	5,064bp
Long16	11,819bp
Long17	8,439bp

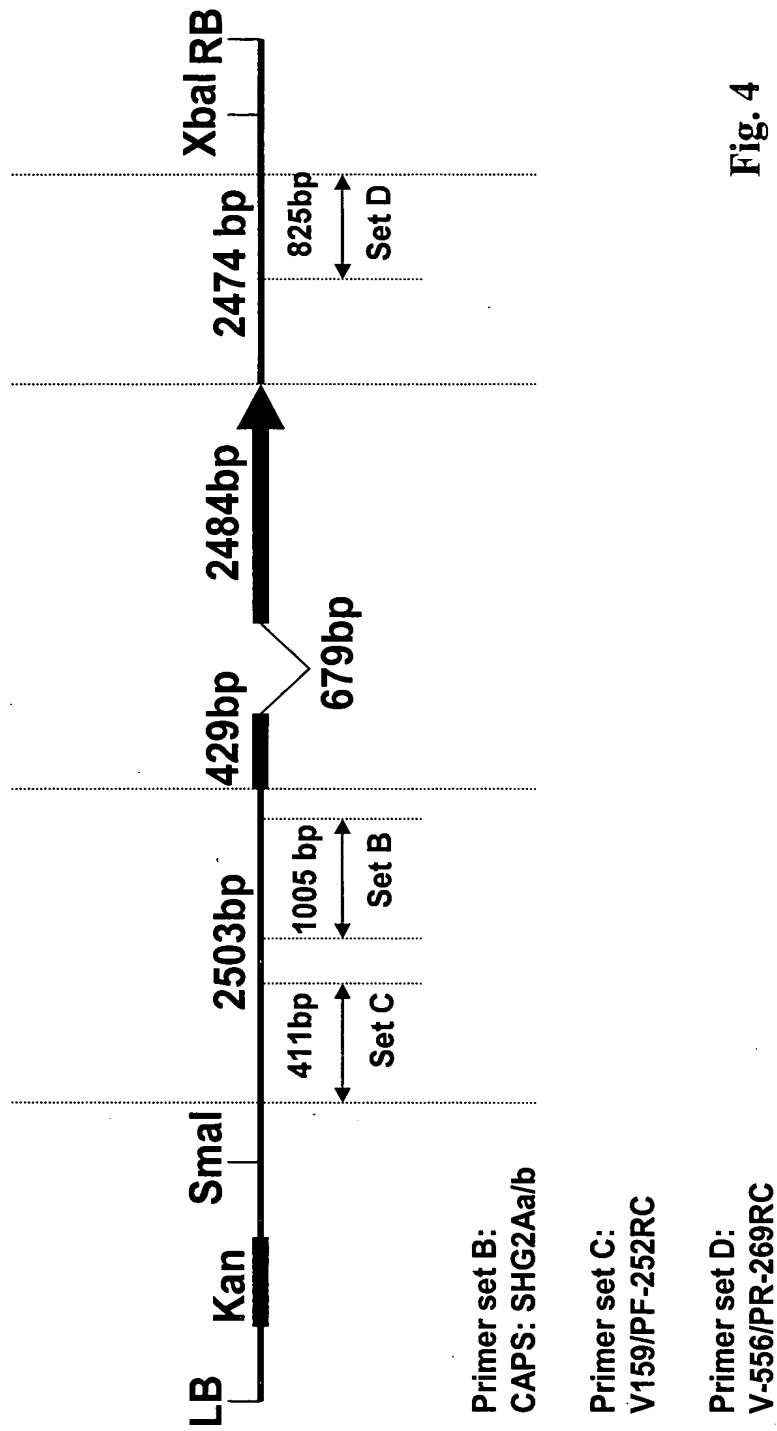


Fig. 4

Map of 2-4-48 (Gene 2, 8,569 bp)

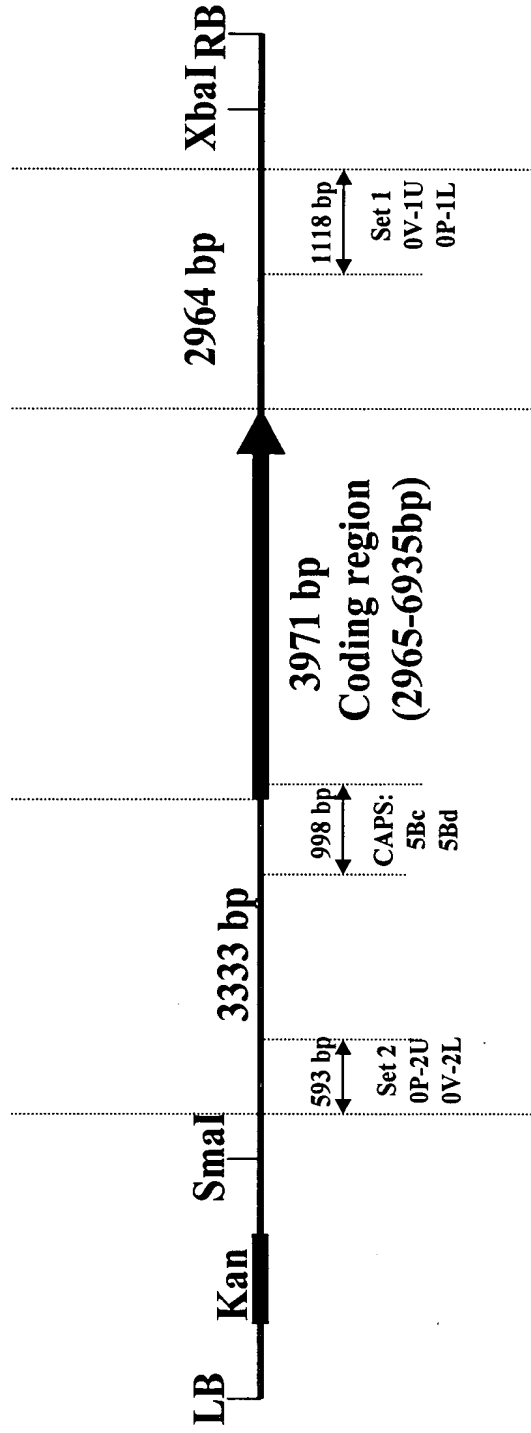


Fig.5

Map of 4B6 (Gene 0, 10,268bp)

Fig. 6a

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RB          DLATSLFSANTSSSNIREINKH-----SYTHMMSIGFAEVVFFYTLPPLKFIISL
RGA1        DLATSLFSANTSSSNIREINAN-----YDGYMMSIGFAEVVSSYSPSLLQKFVSL
RGA3        DLATSMFSASASSRSIRQINVKDDMMFIVTNYKDMMSIGFSEVVSSYSPSLFKRFVSL
RGA4        DLATSLFSASASCGNIREINVK-----DYKHTVSI GFAAVVSSYSPSLLKKFVSL
          *****:****:*. .*:.*: :*****: ** *: . :*:**

RB          RVLNLGDSTFNKLPSSIGDLVHLRYLNLYG-SGMRSLPKQLCKLQNLQTLDLQYCTKLCC
RGA1        RVLNLRNSNLNQLPSSIGDLVHLRYLDLSGNFRIRNLPKRLCKLQNLQTLDLHYCDSLSC
RGA3        RVLNLSNSEFEQLPSSVGDVHLRYLDLSG-NKICSLPKRLCKLQNLQTLDLYNQCSLSC
RGA4        RVLNLSYSKLEQLPSSIGDLLHLRYLDLSC-NNFRSLPERLCKLQNLQTLDVHNCYSLNC
          ***** * :*:****:****:*****:* : .*:*****: * . *

RB          LPKETS KLGSLRNLLDGSQSLTCMPPRIGSLTCLKTLGQFVVGRKKGYQLGELGNLNL
RGA1        LPKQTSKLGSLRNLLLDG-CSLTSTPPRIGLLTCLKSLSCFVIGKRKGHQLGELKNLNL
RGA3        LPKQTSKLC SLRNVLVDH-CPLTSMPPRIGLLTCLKTLGYFVVGERKGYQLGELRNLNL
RGA4        LPKQTSKLSSLRHLVVDG-CPLTSTPPRIGLLTCLKTLGFFIVGSKKGYQLGELKNLNL
          ***:**** ***:***: * ↑ .** .***** ***:***:*. ***: ***:***** **
          720

RB          GSIKISHLERVKNDKDAKEANLSAKGNLHSLSMSWNNFGPHIYESEEVKVLEALKPHSNL
RGA1        GSIKITKLDREVKKDTDAKEANLSAKANLHSLCLSWDLGKHRYDS---EVLEALKPHSNL
RGA3        GAISITHLERVKNDMEAKEANLSAKANLHSLSMSWD--RPNRYESEEVKVLEALKPHPNL
RGA4        GSIITHLERVKNDTDA-EANLSAKANLQSLSMSWDNDGPNRYESKEVKVLEALKPHPNL
          *:***:***:***: * :* *****.***:***:***: * : * * :*****.***
          780

RB          TSLKIYGFRGIHLPEWMNHSVLKNIVSILISNFRNCSCLPFFGDLPCLESLELHWGSADV
RGA1        KYLEINGFGGIRLPDWMNQSVLKNVVSIRIRGCENCSCLPFFGELPCLESLELHTGSADV
RGA3        KYLEIIDFCGFCLPDWMNHSVLKNVVSILISGCENCSCLPFFGELPCLESLELQDGSVEV
RGA4        KYLEIIAFGGFRFPWINHSVLEKVISVRIKCKNCLCLPPFGELPCLENLELQNGSAEV
          . *: * * *: .*:***:***:***:***: * . ** *****:*****.***: ***:
          840

RB          EYVEEVDIDVHSGFPTRIRFPSLRKLDIWDFGSLKGLLKKEGEEQFPVLEEMIIECPFL
RGA1        EYVEDN---VHPG-----RFP SLRKLVIWDFSNLKG LKMEGEKQFPVLEEMTFYWC PMF
RGA3        EYVEDS-----GFLTRRRFPSLRKLHIGGFCNLKGLQRMKGAEQFPVLEEMKISDCPMF
RGA4        EYVEED--DVHSRFFSTRSFPSLKKLRIWFFRSLKGLMKEEGEEKFPMLEEMAILYCLPF
          *****: ▲ *****: * * * .*****: : * :***:*****: * **:
          900

RB          TLS-----SNLRALTSLRICYNKVATSFPEEMFKNLANLKYLT
RGA1        VIPTLSSVKTLKVI-VTDATVLRISNLRALTSLDISDNVEATSLPEEMFKSLANLKYLK
RGA3        VFPTLSSVKKLEIWGEADAGGLSSISNLSTLTSLKIFSNHTVTSLEEMFKNLENLIYLS
RGA4        VFPTLSSVKKLEVHGNTNTRGLSSISNLSTLTSLRIGANYRATSLPEEMFTSLTNLEFLS
          .:.[*****]***:**** * * .*: *****. * ** :*.
          960

RB          ISRCNNLKELPTSLASLNALKSLKIQLCCALES LPEEGLEGLSSLTEL FVEHCNMLKCLP
RGA1        ISFFRN LKELPTSLASLNALKSLKFEFCDALES LPEEGVKGLTSLTELSVSNCMMLKCLP
RGA3        VSFLENLKELPTSLASLN LKCLDIRYCALES LPEEGLEGLSSLTEL FVEHCNMLKCLP
RGA4        FFD FKNLKDLPSTSLTSLNALKRLQIESCDSLESFPEQGLEGLTSLTQLFVKYCKMLKCLP
          . *****:*****:*** ** *: . * :***:***:***:***:***: * * . * *****
          1005

RB          EGLQHLTTLTSLKIRGCPQLIKRCEKGIGEDWHKISHIPNVNIYI
RGA1        EGLQHLTALTTLTITQCPIVFKRCERGIGEDWHKIAHIPYLTLYE
RGA3        EGLQHLTTLTSLKIRGCPQLIKRCEKGIGEDWHKISHIPNVNIYI
RGA4        EGLQHLTALTNLGVSGCPEVEKRCDEIGEDWHKIAHIPNLDIH-
          *****:***: * : * : * : * : *****:***: : :

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Fig. 6b

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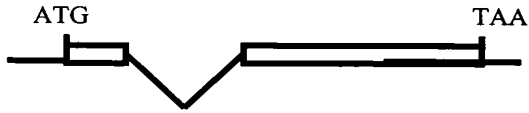


Fig. 7a

MAEAFIQVLLDNLTSFLKGELVLLFGFQDEFQRL
SSMFSTIQAVLEDAQEKQLNNKPLENWLQKLNA
TYEVDDILDEYKTKATRFSSQSEYGRYHPKVIPFR
HKVGKRMDDQVMKKLKAIAEERKNFHLHEKIVERQ
AVRRETGSVLTEPQVYGRDKEKDEIVKILINNVS
DAQHLSVLPILGMGGLGKTTLAQMVFNDRVTEH
FHSKIWICVSEDFDEKRLIKAIVESIEGRPLLGE
MDLAPLQKKLQELLNGKRYLLVLDDVWNEDQQKW
ANLRAVLKVGASGASVLTTRLEKVGSIIMGTLP
YELSNLSQEDCWLFLMQRAGHQQEINPNLVAIG
KEIVKKSQGGVPLAAKTLGGILCFKREERAWEHVR
DSPIWNLPQDESSILPALRLSYHQLPLDLKQCF
YCAVFPKDAKMEKEKLISLWMAHGFLLSKGNMEL
EDVGDEVWKELYLRSSFFQIEVKDGKTYFKMHD
IHDLATSLFSANTSSSNIREINKHSYTHMMSIGF
AEVVFFYTLPP

LEKFISLRVLNLGDSTFNKLPSS
IGDLVHLRYLNLYGSGMRSPLPKQ
LCKLQNLQTLDLQYCTKLCCLPKE
TSKLGSLRNLLLDGSQSLTCMPPRIGS
LTCLKTLGQFVVGRKK
GYQLGELGNLNLYG
SIKISHLERVKNDKDAKEAN
LSAKGNLHSLSMSWNNFGPHIYE
SEEVKVLEALKPHSNLT
SLKIYGFGRGIHLPEWMN
HSVLKNIVSILISNFRNCCLPP
FGDLPCLESLELHWG
SADVEYVEEVDIDVHSGFPT
RIRFPSLRKLDIWDFGSLKGLLKKEG
EEQFPVLEEMIHECPFLTL
SSNLRALTSRLRICYNKVATSFPEEM
FKNLANLKYLTISRNNLKELPTS
LASLNALKSLKIQLCCALESPEEG
LEGLSSLTELFVEHCNMLKCLPEG
LQHLTTLTSLKIRGCPQLIKRCEKGIGED
WHKISHIPNVNIYI

Fig. 7b